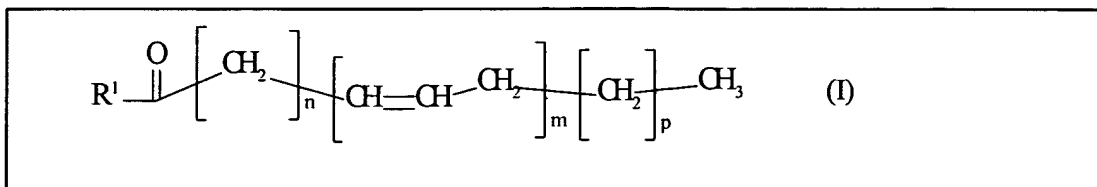


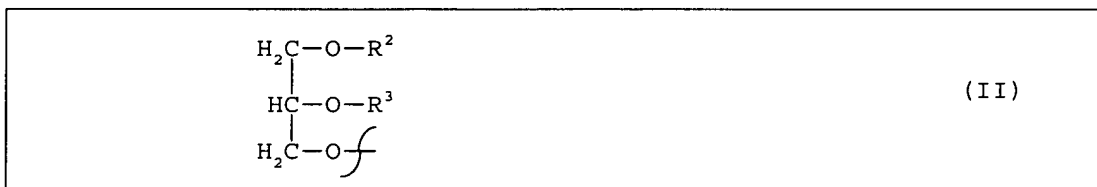
c.) Amendments to the claims.

Please amend claims 1-14 as follows:

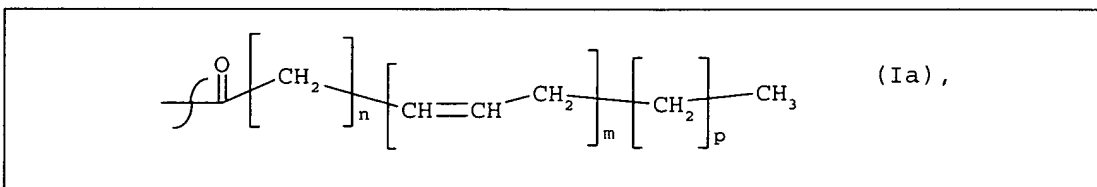
Claim 1. (currently amended) A process for the production of compounds in transgenic plants, wherein said compounds are comprised of the general Formula I:



in transgenic plants with a content of, wherein $\text{R}^1 = -\text{OH}$, coenzyme A (thioester), phosphatidylcholine, phosphatidylethanolamine, phosphatidylglycerol, diphosphatidylglycerol, phosphatidylserine, phosphatidylinositol, sphingolipid, glycosphingolipid or a radical of general Formula II:



wherein $\text{R}^2 = \text{H}$, phosphatidylcholine-, phosphatidylethanolamine-, phosphatidylglycerol-, diphosphatidylglycerol-, phosphatidylserine-, phosphatidylinositol-, sphingolipid-, glycosphingolipid-, glycosphingolipid- or saturated or unsaturated C_2-C_{24} -alkylcarbonyl-; and $\text{R}^3 = \text{H}$, saturated or unsaturated C_2-C_{24} -alkylcarbonyl-; and wherein R^2 and R^3 independently of one another represent a radical of general Formula Ia:



wherein $n = 3, 4$ or 6 ; $m = 3, 4$ or 5 ; and $p = 0$ or 3 , and said compounds comprise at least 1% by weight based on of the total fatty acids acid content of said transgenic plants, which process comprises the following steps:

a) introducing into a plant:

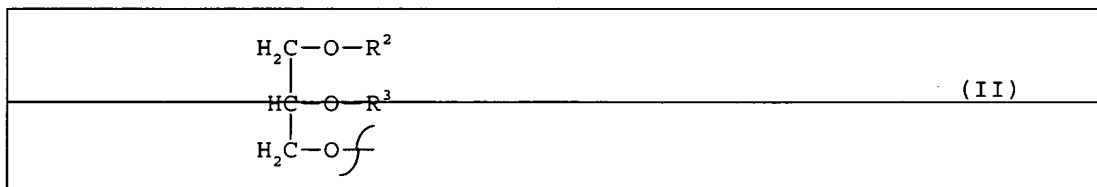
at least one first nucleic acid sequence which encodes a polypeptide with an $\Delta 6$ -desaturase activity; and

b) ~~introducing~~ at least one second nucleic acid sequence which encodes a polypeptide with a $\Delta 6$ -elongase activity; and

c) ~~if appropriate, introducing optionally,~~ a third nucleic acid sequence which encodes a polypeptide with a $\Delta 5$ -desaturase activity; and

d) ~~followed by growing and harvesting the transgenic plant plants; and where the variables and substituents in the formula I have the following meanings:~~

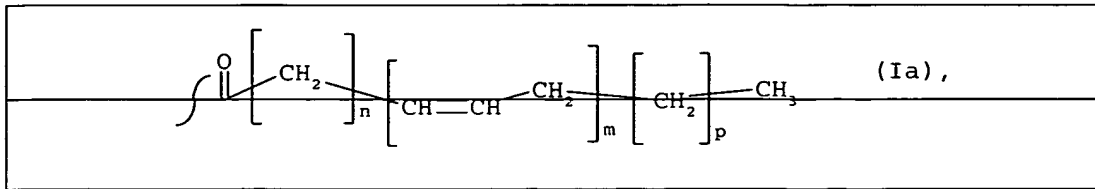
$R^1 = \text{OH}$, coenzyme A (thioester), phosphatidylethanolamine, phosphatidylethanolamine, phosphatidylglycerol, diphosphatidylglycerol, phosphatidylserine, phosphatidylinositol, sphingolipid, glycosphingolipid or a radical of the following general formula II:



$R^2 = \text{H}$, phosphatidylethanolamine, phosphatidylethanolamine, phosphatidylglycerol, diphosphatidylglycerol, phosphatidylserine, phosphatidylinositol, shingolipid, glycosphingolipid, glycosphingolipid or saturated or unsaturated C_2-C_{24} -alkylcarbonyl;

~~— $R^3 = \text{H}$, saturated or unsaturated C_2-C_{24} -alkylcarbonyl; or~~

~~— R^2 and R^3 independently of one another represent a radical of the general formula Ia:~~



$n = 3, 4 \text{ or } 6; m = 3, 4 \text{ or } 5; \text{ and } p = 0 \text{ or } 3.$

Claim 2. (currently amended) The process ~~according to~~ of claim 1, wherein the substituents R^2 and R^3 independently of one another are C_{10} - C_{22} -alkylcarbonyl-.

Claim 3. (currently amended) The process ~~according to~~ of claim 1 ~~or 2~~, wherein the substituents R^2 and R^3 independently of one another are C_{16} -, C_{18} -, C_{20} - or C_{22} -alkylcarbonyl-.

Claim 4. (currently amended) The ~~method according to any of claims 1 to 3~~ process of claim 1, wherein the substituents R^2 and R^3 independently of one another are unsaturated C_{16} -, C_{18} -, C_{20} - or C_{22} -alkylcarbonyl- with one, two, three, four or five double bonds.

Claim 5. (currently amended) The ~~method according to any of claims 1 to 4~~ process of claim 1, wherein the ~~transgenic~~ plant is an oil crop.

Claim 6. (currently amended) The ~~method according to any of claims 1 to 5~~ process of claim 1, wherein the ~~transgenic~~ plant is selected from the group consisting of soya, peanut, oilseed rape, canola, linseed, evening primrose, verbascum, thistle, hazelnut, almond, macadamia, avocado, bay, wild roses, pumpkin/squash, pistachios, sesame, sunflower, safflower, borage, maize, poppy, mustard, hemp, castor-oil plant, olive, Calendula, Punica, oil palm, walnut ~~or~~ and coconut.

Claim 7. (currently amended) The ~~method according to any of claims 1 to 6~~ process of claim 1, wherein the compounds of the general Formula I are obtained from the transgenic plants by pressing or extraction, and said compounds are in the form of their oils, fats, lipids or free fatty acids ~~by pressing or extraction~~.

Claim 8. (currently amended) The ~~process according to any of claims 1 to 7~~ of claim 7, wherein the oils, fats, lipids or free fatty acids ~~obtained as claimed in claim 7~~ are refined.

Claim 9. (currently amended) The ~~process according to any of claims 1 to 8~~ of claim 1, wherein the saturated or unsaturated fatty acids present in the compounds of the ~~formula I~~ are liberated.

Claim 10. (currently amended) The ~~method according to any of claims 1 to 9~~ process of claim 9, wherein the saturated or unsaturated fatty acids are liberated by alkaline hydrolysis or enzymatic cleavage.

Claim 11. (currently amended) The ~~method according to any of claims 1 to 10~~ process of claim 1, wherein the compounds of the ~~general formula I~~ are present in the transgenic plant at a content of comprise at least 5% by weight, ~~based on~~ of the total fatty acids acid content of the transgenic plants.

Claim 12. (currently amended) The ~~process according to any of claims 1 to 11~~ of claim 1, wherein the nucleic acid ~~sequences which encode the polypeptides~~ sequence that encodes the polypeptide with $\Delta 6$ -desaturase activity, $\Delta 6$ -elongase activity or $\Delta 5$ -desaturase activity ~~are~~ is selected from the group consisting of:

a) a nucleic acid sequence with that contains the sequence shown in of SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29 or SEQ ID NO: 31,

b) nucleic acid sequences which, owing to the degeneracy of the genetic code, are obtained by back translation of the an amino acid ~~sequences shown in~~ sequence contains the sequence of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30 or SEQ ID NO: 32,

c) derivatives of ~~the a~~ nucleic acid ~~sequences shown in~~ sequence that contains the sequence of SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29 or SEQ ID NO: 31, which encode ~~polypeptides with the a~~ derivative polypeptide that contains the amino acid ~~sequences shown in~~ sequence of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30 or SEQ ID NO: 32, and which ~~have~~ has at least 50% homology at the amino acid level, ~~without the wherein~~ enzymatic activity of the derivative polypeptide ~~being is not~~ substantially reduced as compared to said polypeptide.

Claim 13. (currently amended) The process ~~according to any of claims 1 to 12 of~~ claim 1, wherein one or more of the first, second, and optionally third nucleic acid sequences ~~as claimed in claim 8~~ are linked with one or more regulatory signals in a nucleic acid construct.

Claim 14. (currently amended) The ~~method according to any of claims 1 to 13~~ process of claim 13, wherein the nucleic acid construct comprises additional biosynthetic genes of the fatty acid or lipid metabolism selected from the group consisting of acyl-CoA dehydrogenase(s), acyl-ACP [= acyl carrier protein] desaturase(s), acyl-ACP thioesterase(s), fatty acid acyl transferase(s), fatty acid synthase(s), fatty acid hydroxylase(s), acetyl-coenzyme A carboxylase(s), acyl-coenzyme A oxidase(s), fatty acid desaturase(s), fatty acid acetylenases, lipoxygenases, triacylglycerol lipases, allene oxide synthases, hydroperoxide lyases, ~~or~~ fatty acid elongase(s) and combinations thereof.

Please add the following as new claims 15-20:

Claim 15. (new) The process of claim 1, wherein the first, second and optionally third nucleic acid sequences are stably integrated in the plant.

Claim 16. (new) The process of claim 1, wherein the plant is selected from the group consisting of plant cells, plant tissues, plant organs, plant leaves, plant roots, plant stems, intact plants, plant tubers, plant seeds, and cellular parts of any of the preceding.

Claim 17. (new) The process of claim 7, wherein the pressing or the extraction is performed without supplying heat.

Claim 18. (new) The process of claim 12, wherein two or more of the first, second and third nucleic acid sequences are selected from said group.

Claim 19. (new) The process of claim 12, wherein the first, second and third nucleic acid sequences are selected from said group.

Claim 20. (new) The process of claim 13, wherein the first, second and third nucleic acid sequences are linked to with one or more regulatory signals in said nucleic acid construct.